

- 1 -
piece 1, NC 000913, fnr ogt+, config: linear, direction: +, begin: 1397521, end: 1397764

The figure shows a genomic sequence from position 5' to 3'. Above the sequence, gene start sites are marked with asterisks (*). Below the sequence, amino acid translations are shown for each gene. Red dots indicate specific mutations or features of interest.

Genes labeled:

- * 1397530
- * 1397540
- * 1397550
- * 1397560
- * 1397570
- * 1397580
- * 1397590
- * 1397600

Sequence details:

- Gene 1397530:** ala - pro - tyr - asn - ser - leu - phe - arg - asp - his - arg - ser - ala - gln - ala - val - ile - asp - ile - cys - gln - phe - .
- Gene 1397540:** - arg - arg - ile - ile - arg - phe - ser - gly - ile - ile - gly - leu - leu - lys - pro - .
- Gene 1397550:** - fMet - ile - phe - val - asn - phe - asn - ile - phe - leu - gly -
- Gene 1397560:** - ala - val - .
- Gene 1397570:** - fMet - ile - phe - val - asn - phe - ser - ile - leu - thr - ser - phe - .
- Gene 1397580:** - fMet - ser - ile - leu - thr - ser - phe - .
- Gene 1397590:** - ala - cat - ttt - tt - tagg - 3'
- Gene 1397600:** ...

Red dots are located at positions 1397530: 1397530, 1397540: 1397540, 1397550: 1397550, 1397560: 1397560, 1397570: 1397570, 1397580: 1397580, 1397590: 1397590, and 1397600: 1397600.

5' g a g c a a g t a a g t c t a a g c a a a c c t t a a c a g c a g a a t t c c g a t a t t a g a t g t a a a t a t a t g t c t a t c t a t t g a a a a a c c c 3'

- ser - lys - fMet -

fMet ser ile tvr leu lys thr leu

ir fnr_ogt+

Detailed description: This is a genomic map showing transcription start sites (TSS) indicated by red arrows pointing left. A green box labeled 'sd' represents a promoter. A purple box labeled 'p35' represents a gene. Brackets indicate genomic regions: 'sd-(8)-ir 1397661 Gap 2.4 bits' and 'sd-ir 1397661 fnr out+ total 5.9 bits'. A large bracket covers the p35 gene with a label 'p35 2.5 bits'. Another bracket covers the p35 gene and a gap with a label 'p35-(25)-p10 1397699 Gap'. Below the p35 gene, another bracket indicates 'p35 6.4 bits'. Total lengths for some regions are given as '... p35-(23)-p10 1397685 Gap', '... p35-p10 1397685 total 4.1', and '... p35-p10 1397699 total 6.1'.

Sequence alignment showing two p10 variants with 3.8 bits and 3.7 bits of conservation. The sequence starts with fMet and ends with fMet. A red circle highlights a difference at position 1397760.

... -----} p35-(25)-p10 1397699 Gap 4.0 bits

Diagram illustrating protein fragments p35 and p10 with their codon usage bar charts and sequence alignment.

p35 4.8 bits

p10 4.5 bits

**{ p35-(24)-p10 1397759 Gap 2.4 bits
p35-p10 1397759 total 6.8 bits }**

... ----- } p35-(23)-p10 1397685 Gap 1.4 bits
... ----- } p35-p10 1397685 total 4.9 bits

... -----| p35-p10 1397699 total 6.1 bits

5' t 3'

... -- ... NC_000913.ogt